RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/764,131_

Source: _____

Date Processed by STIC: _____

ENTERED

IFWO

RAW SEQUENCE LISTING   DATE: 03/09/2005
PATENT APPLICATION: US/10/764,131   TIME: 09:51:18

Input Set : **N:\Crf3\RULE60\10764131.raw.txt**
Output Set: **N:\CRF4\03092005\J764131.raw**

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 1 <110> APPLICANT: KELER, Tibor
 2        GOLDSTEIN, Joel
 3        GRAZIANO, Robert
 4        DEO, Yashwant M.
 5 <120> TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
 6        BINDING COMPONENTS
 7 <130> FILE REFERENCE: MXI-099CPA
 8 <140> CURRENT APPLICATION NUMBER: US/10/764,131
 9 <141> CURRENT FILING DATE: 2004-01-23
10 <150> PRIOR APPLICATION NUMBER: US/09/203,958
11 <151> PRIOR FILING DATE: 1998-12-02
12 <150> PRIOR APPLICATION NUMBER: 60/067232
13 <151> PRIOR FILING DATE: 1997-12-02
14 <160> NUMBER OF SEQ ID NOS: 4
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1132
19 <212> TYPE: DNA
20 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Synthetic construct
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (74)...(1129)
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27      aagcttggta ccgagctcgg atccactagt aacggccgcc agtgtgctgg aattcggctt 60
28      ggggatatcc acc atg gag aca gac aca ctc ctg cta tgg gta ctg ctg     109
29                  Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu
30                   1               5                  10
31      ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat     157
32      Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp
33              15                  20                  25
34      tat gct ggg gcc cag ccg gcc aga tct gat atc cag ctg acc cag agc     205
35      Tyr Ala Gly Ala Gln Pro Ala Arg Ser Asp Ile Gln Leu Thr Gln Ser
36          30                  35                  40
37      cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt     253
38      Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
39      45                  50                  55                  60
40      aag tcc agt caa agt gtt tta tac agt tca aat cag aag aac tac ttg     301
41      Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
42                      65                  70                  75
43      gcc tgg tac cag cag aag cca ggt aag gct cca aag ctg ctg atc tac     349
44      Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
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45                 80                  85                    90
46    tgg gca tcc act agg gaa tct ggt gtg cca agc aga ttc agc ggt agc    397
47    Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
48            95                  100                   105
49    ggt agc ggt acc gac ttc acc ttc acc atc agc agc ctc cag cca gag    445
50    Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
51            110                 115                   120
52    gac atc gcc acc tac tac tgc cat caa tac ctc tcc tcg tgg acg ttc    493
53    Asp Ile Ala Thr Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe
54    125                 130                 135                   140
55    ggc caa ggg acc aag gtg gaa atc aag agc tct ggc ggt ggc ggc tcc    541
56    Gly Gln Gly Thr Lys Val Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser
57            145                 150                   155
58    gga ggt gga ggc agc gga ggg ggt gga tcc gag gtc caa ctg gtg gag    589
59    Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
60            160                 165                   170
61    agc ggt gga ggt gtt gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc    637
62    Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys
63            175                 180                   185
64    tcc tcg tct ggc ttc att ttc agt gac aat tac atg tat tgg gtg aga    685
65    Ser Ser Ser Gly Phe Ile Phe Ser Asp Asn Tyr Met Tyr Trp Val Arg
66            190                 195                   200
67    cag gca cct gga aaa ggt ctt gag tgg gtt gca acc att agt gat ggt    733
68    Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Gly
69    205                 210                 215                   220
70    ggt agt tac acc tac tat cca gac agt gtg aag gga aga ttt aca ata    781
71    Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile
72            225                 230                   235
73    tcg aga gac aac agc aag aac aca ttg ttc ctg caa atg gac agc ctg    829
74    Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu
75            240                 245                   250
76    aga ccc gaa gac acc ggg gtc tat ttt tgt gca aga ggc tac tat agg    877
77    Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Arg Gly Tyr Tyr Arg
78            255                 260                   265
79    tac gag ggg gct atg gac tac tgg ggc caa ggg acc ccg gtc acc gtc    925
80    Tyr Glu Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val
81    270                 275                 280
82    tcc tca ccg cgg ctg cag gtc gac gaa caa aaa ctc atc tca gaa gag    973
83    Ser Ser Pro Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu
84    285                 290                 295                   300
85    gat ctg aat gct gtg ggc cag gac acg cag gag gtc atc gtg gtg cca    1021
86    Asp Leu Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro
87            305                 310                   315
88    cac tcc ttg ccc ttt aag gtg gtg gtg atc tca gcc atc ctg gcc ctg    1069
89    His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu
90            320                 325                   330
91    gtg gtg ctc acc atc atc tcc ctt atc atc ctc atc atg ctt tgg cag    1117
92    Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln
93            335                 340                   345
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RAW SEQUENCE LISTING   DATE: 03/09/2005
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Input Set : N:\Crf3\RULE60\10764131.raw.txt
Output Set: N:\CRF4\03092005\J764131.raw

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94          aag aag cca cgt tag                                                   1132
95          Lys Lys Pro Arg
96              350
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 352
100 <212> TYPE: PRT
101 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Synthetic construct
104 <400> SEQUENCE: 2
105         Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
106          1               5                  10                  15
107         Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
108                     20                  25                  30
109         Gln Pro Ala Arg Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu
110                 35                  40                  45
111         Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln
112             50                  55                  60
113         Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln
114         65                  70                  75                  80
115         Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
116                     85                  90                  95
117         Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
118                     100                 105                 110
119         Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr
120                     115                 120                 125
121         Tyr Tyr Cys His Gln Tyr Leu Ser Ser Trp Thr Phe Gly Gln Gly Thr
122             130                 135                 140
123         Lys Val Glu Ile Lys Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
124         145                 150                 155                 160
125         Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly
126                     165                 170                 175
127         Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ser Ser Gly
128                     180                 185                 190
129         Phe Ile Phe Ser Asp Asn Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly
130                     195                 200                 205
131         Lys Gly Leu Glu Trp Val Ala Thr Ile Ser Asp Gly Gly Ser Tyr Thr
132             210                 215                 220
133         Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
134         225                 230                 235                 240
135         Ser Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp
136                     245                 250                 255
137         Thr Gly Val Tyr Phe Cys Ala Arg Gly Tyr Tyr Arg Tyr Glu Gly Ala
138                     260                 265                 270
139         Met Asp Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Pro Arg
140                     275                 280                 285
141         Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala
142             290                 295                 300
143         Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu Pro
```

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144        305                      310                      315                      320
145        Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr
146                            325                      330                      335
147        Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg
148                        340                      345                      350
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 1135
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Synthetic construct
156 <220> FEATURE:
157 <221> NAME/KEY: CDS
158 <222> LOCATION: (74)...(1132)
159 <400> SEQUENCE: 3
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161        ggggatatcc acc atg gag aca gac aca ctc ctg cta tgg gta ctg ctg      109
162                    Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu
163                    1               5                      10
164        ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat   157
165        Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp
166                    15                  20                  25
167        tat gct ggg gcc cag ccg gcc aga tct gag atc cag ctg cag cag act   205
168        Tyr Ala Gly Ala Gln Pro Ala Arg Ser Glu Ile Gln Leu Gln Gln Thr
169                30                  35                  40
170        gga cct gag ctg gtg aag cct ggg gct tca gtg aag ata tcc tgc aag   253
171        Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys
172            45                  50                  55                  60
173        gct tct ggt tat tca ttc act gac tac atc ata ttt tgg gtg aag cag   301
174        Ala Ser Gly Tyr Ser Phe Thr Asp Tyr Ile Ile Phe Trp Val Lys Gln
175                        65                  70                  75
176        agc cat gga aag agc ctt gag tgg act gga aat aat aat cct tac tat   349
177        Ser His Gly Lys Ser Leu Glu Trp Thr Gly Asn Asn Asn Pro Tyr Tyr
178                    80                  85                  90
179        ggt agt act agc tac aat ctg aag ttc aag ggc aag gcc aca ttg act   397
180        Gly Ser Thr Ser Tyr Asn Leu Lys Phe Lys Gly Lys Ala Thr Leu Thr
181                    95                  100                 105
182        gta gac aaa tct tcc agc aca gcc tac atg cag ctc aac agt ctg aca   445
183        Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr
184            110                 115                 120
185        tct gag gac tct gca gtc tat tac tgt gta aga gga gtt tat tac tac   493
186        Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Arg Gly Val Tyr Tyr Tyr
187        125                 130                 135                 140
188        ggt agt agc tac gag gcg ttt cct tac tgg ggc caa ggg act ctg gtc   541
189        Gly Ser Ser Tyr Glu Ala Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val
190                        145                 150                 155
191        act gtc tct gca gga ggt ggc ggc tcc gga gga ggt ggc agc gga ggg   589
192        Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
193                    160                 165                 170
```

```
194        ggc gga tcc gat gtt gtg atg acc cag act cca ctc act ttg tcg att    637
195        Gly Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Ile
196                175                    180                    185
197        acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc ctc    685
198        Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
199                190                    195                    200
200        tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg cca    733
201        Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
202        205                    210                    215                220
203        ggc cag tct cca acg cgc cta atc tat ctg gtg tct aaa ctg gac tct    781
204        Gly Gln Ser Pro Thr Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
205                225                    230                    235
206        gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttc aca    829
207        Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
208                240                    245                    250
209        ctg aaa atc agc aga gtg gag gct gag gat ttg gga att tat tat tgc    877
210        Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
211                255                    260                    265
212        tgg caa ggt gca cat ttt cct cag acg ttc ggt gga ggc acc aag ctg    925
213        Trp Gln Gly Ala His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu
214                270                    275                    280
215        gaa atc aaa ccg cgg ctg cag gtc gac gaa caa aaa ctc atc tca gaa    973
216        Glu Ile Lys Pro Arg Leu Gln Val Asp Glu Gln Lys Leu Ile Ser Glu
217        285                    290                    295                300
218        gag gat ctg aat gct gtg ggc cag gac acg cag gag gtc atc gtg gtg    1021
219        Glu Asp Leu Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val
220                305                    310                    315
221        cca cac tcc ttg ccc ttt aag gtg gtg gtg atc tca gcc atc ctg gcc    1069
222        Pro His Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala
223                320                    325                    330
224        ctg gtg gtg ctc acc atc atc tcc ctt atc atc ctc atc atg ctt tgg    1117
225        Leu Val Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp
226                335                    340                    345
227        cag aag aag cca cgt tag                                            1135
228        Gln Lys Lys Pro Arg
229                350
231 <210> SEQ ID NO: 4
232 <211> LENGTH: 353
233 <212> TYPE: PRT
234 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Synthetic construct
237 <400> SEQUENCE: 4
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239        1                    5                    10                    15
240        Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala
241                20                    25                    30
242        Gln Pro Ala Arg Ser Glu Ile Gln Leu Gln Gln Thr Gly Pro Glu Leu
243                35                    40                    45
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VERIFICATION SUMMARY　　　　　　　　DATE: 03/09/2005
PATENT APPLICATION:　**US/10/764,131**　　TIME: 09:51:19

Input Set : **N:\Crf3\RULE60\10764131.raw.txt**
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